

The following Listing of the Claims will replace all prior versions and all prior listings of the claims in the present application:

1.-63. (Cancelled)

64. (New) A method of identifying two or more markers useful for diagnosing a disease, the method comprising:

for each gene of a collection of two or more genes, wherein the gene is expressed in blood and in a non-blood tissue of a subject not having the disease;

(a) using an oligonucleotide of predetermined sequence, detecting a presence, in RNA isolated from blood samples which have not been fractionated into cell types from subjects having the disease, of RNA encoded by the gene, the oligonucleotide being specific for RNA encoded only by the gene, and/or for cDNA complementary to RNA encoded only by the gene, in the samples;

(b) quantifying a level of RNA encoded by the gene in the samples; and

(c) determining a difference between the level, and a quantified level of RNA encoded by the gene in RNA isolated from blood samples which have not been fractionated into cell types from control subjects, RNA encoded by the gene having been detected in the samples from the control subjects, and the difference identifying the gene as a marker of the disease,

thereby identifying two or more markers useful for diagnosing a disease.

65. (New) A method of identifying two or more markers of a disease, the method comprising:

for each gene of a collection of two or more genes, wherein the gene is expressed in blood and in a non-blood tissue of a subject not having the disease;

(a) using an oligonucleotide of predetermined sequence, detecting a presence, in RNA isolated from samples of whole blood from subjects having the disease, of RNA encoded by the gene, the oligonucleotide being specific for RNA encoded only by the gene, and/or for cDNA complementary to RNA encoded only by the gene, in the samples;

(b) quantifying a level of RNA encoded by the gene in the samples; and

(c) determining a difference between the level, and a quantified level of RNA encoded by the gene in RNA isolated from samples of whole blood from control subjects, RNA encoded by the gene having been detected in the samples from the control subjects, and the difference identifying the gene as a marker of the disease,

thereby identifying two or more potential markers of a disease.

66. (New) A method of identifying two or more markers useful for diagnosing a disease, the method comprising:

for each gene of a collection of two or more genes, wherein the gene is expressed in blood and in a non-blood tissue of a subject not having the disease:

(a) producing amplification products from RNA of blood samples which have not been fractionated into cell types from subjects having the disease, using primers specific for RNA encoded only by the gene, and/or for cDNA complementary to RNA encoded only by the gene, in the sample;

(b) quantifying a level of the amplification products; and

(c) determining a difference between the level and a quantified level of control amplification products produced from control RNA, using primers specific for RNA encoded only by the gene, and/or for cDNA complementary to RNA encoded only by the gene, in RNA of blood samples which have not been fractionated into cell types from control subjects, wherein the difference identifies the gene as a marker of the disease,

thereby identifying two or more potential markers useful for diagnosing a disease.

67. (New) A method of identifying two or more markers of a disease, the method comprising:

for each gene of a collection of two or more genes, wherein the gene is expressed in blood and in a non-blood tissue of a subject not having the disease:

(a) producing amplification products from RNA of samples of whole blood from subjects having the disease, using primers specific for RNA encoded only by the gene, and/or for cDNA complementary to RNA encoded only by the gene, in the sample;

(b) quantifying a level of the amplification products; and

(c) determining a difference between the level and a quantified level of control amplification products produced from control RNA, using primers specific for RNA encoded only by the gene, and/or for cDNA complementary to RNA encoded only by the gene, in RNA of samples of whole blood from control subjects, wherein the difference identifies the gene as a marker of the disease,

thereby identifying two or more potential markers of a disease.

68. (New) The method of claim 64 or 65, wherein the detecting of RNA encoded by the gene in step (a) is effected by detecting cDNA and/or EST derived from RNA encoded by the gene .
69. (New) The method of claim 66 or 67, wherein the producing of the amplification products in step (a) is effected by producing amplification products from cDNA and/or EST derived from RNA encoded by the gene.
70. (New) The method of claim 64 or 65, further comprising quantifying a level of RNA encoded by the gene in the RNA of the blood samples from the control subjects, to thereby determine the quantified level of RNA encoded by the gene in RNA of the blood samples from the control subjects.
71. (New) The method of claim 66 or 67, further comprising quantifying a level of the control amplification products to thereby determine the quantified level of the control amplification products.
72. (New) The method claim 64 or 65, wherein the quantifying of the level of RNA encoded by the gene in step (b) is effected by determining a quantity of RNA encoded by the gene in the RNA of the blood samples from the subjects not having the disease relative to a housekeeping gene.
73. (New) The method of claim 64 or 65, wherein the quantified level of RNA encoded by the gene in RNA of the blood samples from the control subjects has been determined relative to a housekeeping gene.
74. (New) The method of claim 66 or 67, wherein the quantified level of control amplification products has been determined relative to a housekeeping gene.
75. (New) The method of claim 64, 65, 66 or 67, wherein the control subjects and the subjects having the disease are human.

76. (New) The method of claim 64, 65, 66 or 67, wherein the control subjects do not have the disease.
77. (New) The method of claim 66 or 67, wherein the quantifying of the level of the amplification products in step (b) is effected by quantifying amplification products produced from cDNA and/or EST derived from RNA encoded by the gene .
78. (New) The method of claim 64 or 65, wherein the quantifying of the level of RNA encoded by the gene in step (b) is effected by quantifying a level of cDNA and/or EST derived from RNA encoded by the gene.
79. (New) The method of claim 64, 65, 66 or 67, wherein the disease is colorectal cancer.
80. (New) The method of claim 64, 65, 66 or 67, wherein the control subjects have the disease at a different stage than the subjects having the disease.
81. (New) The method of claim 66 or 67, wherein the quantifying of the level of the amplification products in step (b) is effected by determining a quantity of the amplification products produced from the RNA of the blood samples from the subjects having the disease relative to a housekeeping gene.
82. (New) The method of claim 64, 65, 66 or 67, wherein the disease is diabetes.
83. (New) The method of claim 64, 65, 66 or 67, wherein the disease is heart failure.
84. (New) The method of claim 64, 65, 66 or 67, wherein the gene is predominantly expressed in the non-blood tissue.
85. (New) The method of claim 64, 65, 66 or 67, wherein the marker is a potential marker.
86. (New) The method of claim 64, 65, 66 or 67, wherein the gene is non-cancer-associated.